

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Tang, Y. Tom
- (ii) TITLE OF THE INVENTION: NEW SYNAPTOJANIN ISOFORM
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/904,234
 - (B) FILING DATE: July 31,1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0357-1 DIV
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: SYNORAT01
 - (B) CLONE: 367401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Pro Gln Ser Gly Pro Gln Pro Asn Leu Glu Thr Pro Pro Gln Pro
 1 5 10 15
 Pro Pro Arg Ser Arg Ser Ser His Ser Leu Pro Ser Glu Ala Ser Ser
 20 25 30
 Gln Pro Gln Val Lys Thr Asn Gly Ile Ser Asp Gly Lys Arg Glu Ser
 35 40 45
 Pro Leu Lys Ile Asp Pro Phe Glu Asp Leu Ser Phe Asn Leu Leu Ala
 50 55 60
 Val Ser Lys Ala Gln Leu Ser Val Gln Thr Ser Pro Val Pro Thr Pro
 65 70 75 80
 Asp Pro Lys Arg Leu Ile Gln Leu Pro Ser Ala Thr Gln Ser Asn Val
 85 90 95
 Asn Thr Leu Ser Ser Val Ser Cys Met Pro Thr Met Pro Pro Ile Pro
 100 105 110
 Ala Arg Ser Gln Ser Gln Glu Asn Met Arg Ser Ser Pro Asn Pro Phe
 115 120 125
 Ile Thr Gly Leu Thr Arg Thr Asn Pro Phe Ser Asp Arg Thr Ala Ala
 130 135 140
 Pro Gly Asn Pro Phe Arg Ala Lys Ser Glu Glu Ser Glu Ala Thr Ser
 145 150 155 160
 Trp Phe Ser Lys Glu Pro Val Thr Ile Ser Pro Phe Pro Ser Leu
 165 170 175
 Gln Pro Leu Gly His Asn Lys Ser Arg Ala Ser Ser Ser Leu Asp Gly
 180 185 190
 Phe Lys Asp Ser Phe Asp Leu Gln Gly Gln Ser Thr Leu Lys Ile Ser
 195 200 205
 Asn Pro Lys Gly Trp Val Thr Phe Glu Glu Glu Glu Asp Phe Gly Val
 210 215 220
 Lys Gly Lys Ser Lys Ser Ala Cys Ser Asp Leu Leu Gly Asn Gln Pro
 225 230 235 240
 Ser Ser Phe Ser Gly Ser Asn Leu Thr Leu Asn Asp Asp Trp Asn Lys
 245 250 255
 Gly Thr Asn Val Ser Phe Cys Val Leu Pro Ser Arg Arg Pro Pro Pro
 260 265 270
 Pro Pro Val Pro Leu Leu Pro Pro Gly Thr Ser Pro Pro Val Asp Pro
 275 280 285
 Phe Thr Thr Leu Ala Ser Lys Ala Ser Pro Thr Leu Asp Phe Thr Glu
 290 295 300
 Arg
 305

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT01
- (B) CLONE: 367401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGTGTACAG CGTCCGGTCG ACAGGTTCAA CTTTCCTTCC TGAACCACTG AAGCCTCAGG 60
 CTGCTTTTCC TCCGCGGTCT TCTTTGCGCC CGCCTGCTCA AAGGTTGCAA GAGCCTCTTG 120
 TCCCTGTGGC AGCACCTATG CCTCAGTCTG GCCCCAGCC AAATTTGGAA ACCCCACCAC 180
 AACCACCACC TCGAAGCAGG TCATCCCATA GCTTGCCTTC AGAAGCTTCC TCACAACCGC 240

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AAGTAAAAAC AAATGGAATC TCTGATGGCA AAAGAGAATC ACCATTAAAG ATTGACCCAT 300
TTGAAGATCT GTCATTTAAT CTGCTTGCTG TATCAAAGGC TCAGCTATCT GTTCAAACGT 360
CACCTGTTCC CACCCCAGAC CCAAAGAGGT TGATTCAGTT GCCTTCTGCA ACGCAAAGTA 420
ATGTTAATAC TTTGAGTTCT GTAAGTTGCA TGCCAACAAT GCCTCCAATT CCAGCTCGGA 480
GTCAATCCCA GGAAAATATG CGAAGTTCTC CAAACCCATT TATTACTGGC TTGACCAGGA 540
CAAATCCTTT CAGTGACAGG ACTGCTGCTC CTGGAAACCC ATTTAGAGCC AAGTCTGAAG 600
AATCAGAGGC AACTTCATGG TTCTCCAAAG AAGAGCCCGT TACTATCAGT CCTTTCCCTT 660
CTCTGCAGCC TCTTGGTCAT AACAAAAGCA GGGCTTCATC TTCACTTGAT GGCTTTAAGG 720
ACAGTTTTGA TCTACAGGGC CAGTCTACAT TAAAAATTAG CAACCCGAAA GGATGGGTAA 780
CCTTCGAGGA AGAAGAGGAT TTTGGTGTGA AAGGGAAGTC AAAGTCAGCT TGTTTCAGACT 840
TACTGGGTAA TCAGCCAAGT TCATTTTCTG GCTCCAACCT GACATTGAAT GATGACTGGA 900
ATAAAGGTAC AAATGTCTCC TTCTGTGTGT TGCCGTCAAG AAGACCTCCT CCACCTCCTG 960
TCCCTCTGCT CCCGCCCGGC ACCAGCCCTC CAGTAGATCC TTTCACGACC TTGGCCTCTA 1020
AGGCTTCACC CACACTGGAC TTTACAGAAA GATAACGCCA TGCAATAGAA AACAGTGGGT 1080
ACTTGCTTTT GGCAGGATAG AGCTAAGAGA ATTGGGCATT AGTATTTTCA TATGTGCAAT 1140
AAGTCATTGT AAGTGCACCT ATATCTTCAC AAAACACCAC TATTTGATGT GTACAGAGTT 1200
GGACTATGTG TATATTGGAA ATAAGGAAAA ACCCTTCTCA TTGTTAACTG GAGTTTGTAT 1260
GTATTTCTCT TTGGATGAAT AGGAGACAGT AGTAGCCATA AAAAGTACTT ATACTTTAGA 1320
AAACAGTCCT TATTCAGAAA CTTTTCGGTC AGTCTTCTGA AGAATCTCAA AAAGCCCACC 1380
CAACTTTTCA GCTGACATTT CCACCAGCCC TCTCAAATTT GTTAACTATT GGTATCTTTG 1440
AGTATTTACC CAAGAGCTGC CAAGGTTACA GTGAACAGAG TTTTGAAAGG CATTGCTTTA 1500
AAGGAAAAAA GTATAGGTAT GTGTACATAT ANATTTTATA TTTTCACACG TACTTCCGTC 1560
CCCC

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1166576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Gln Gln Val Lys Ile Asn Gly Ala Cys Gly Val Lys Gln Glu Pro Thr
 1          5          10          15
Leu Lys Ser Asp Pro Phe Glu Asp Leu Ser Leu Ser Val Leu Ala Val
 20          25          30
Ser Lys Ala Gln Pro Ser Ala Gln Ile Ser Pro Val Leu Thr Pro Asp
 35          40          45
Pro Lys Met Leu Ile Gln Leu Pro Ser Ala Ser Gln Ser Lys Val Asn
 50          55          60
Ser Leu Ser Ser Val Ser Cys Met Leu Thr Met Pro Pro Val Pro Glu
 65          70          75          80
Gln Ser Lys Ser Gln Glu Ser Val Gly Ser Ser Ala Asn Pro Phe Pro
 85          90          95
Ser Leu Pro Thr Arg Asn Pro Phe Thr Asp Arg Thr Ala Ala Pro Gly
100          105          110
Asn Pro Phe Arg Val Gln Ser Gln Glu Ser Glu Ala Thr Ser Trp Leu
115          120          125
Ser Lys Glu Glu Pro Val Ser Asn Ser Pro Phe Pro Pro Leu Met Pro
130          135          140
Leu Ser His Asp Met Ser Lys Pro Ser Ser Ser Leu Asp Gly Phe Glu
145          150          155          160
Asp Asn Phe Asp Leu Gln Ser Gln Ser Thr Val Lys Thr Ser Asn Pro
165          170          175

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[illegible]

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